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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/824,286

DATE: 04/17/2001

TIME: 10:47:23

Input Set : A:\A006p.txt

Output Set: N:\CRF3\04172001\I824286.raw

## SEQUENCE LISTING

ENTERED

## 4 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Burkly, Linda C  
 6 Benjamin, Christopher D  
 7 Hession, Catherine A  
 8 Whitty, Adrian

9 (ii) TITLE OF INVENTION: COMMON GAMMA CHAIN BLOCKING AGENTS

10 (iii) NUMBER OF SEQUENCES: 17

11 (iv) CORRESPONDENCE ADDRESS:

12 (A) ADDRESSEE: Biogen, Inc.  
 13 (B) STREET: 14 Cambridge Center  
 14 (C) CITY: Cambridge  
 15 (D) STATE: Massachusetts  
 16 (E) COUNTRY: USA  
 17 (F) ZIP: 02142

18 (v) COMPUTER READABLE FORM:

19 (A) MEDIUM TYPE: Floppy disk  
 20 (B) COMPUTER: IBM PC compatible  
 21 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 22 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

23 (vi) CURRENT APPLICATION DATA:

24 (A) APPLICATION NUMBER: US/09/824,286  
 25 (B) FILING DATE: 02-Apr-2001  
 26 (C) CLASSIFICATION:

27 (vii) PRIOR APPLICATION DATA:

28 (A) APPLICATION NUMBER: 60/017,466  
 29 (B) FILING DATE: 10-MAY-1996

30 (viii) ATTORNEY/AGENT INFORMATION:

31 (A) NAME: Kaplan, Warren A.  
 32 (B) REGISTRATION NUMBER: 34,199  
 33 (C) REFERENCE/DOCKET NUMBER: A006 PCT CIP

34 (ix) TELECOMMUNICATION INFORMATION:

35 (A) TELEPHONE: 617 679-2000  
 36 (B) TELEFAX: 617 679-2838

37 (2) INFORMATION FOR SEQ ID NO: 1:

38 (i) SEQUENCE CHARACTERISTICS:

39 (A) LENGTH: 1446 base pairs  
 40 (B) TYPE: nucleic acid  
 41 (C) STRANDEDNESS: single  
 42 (D) TOPOLOGY: linear

43 (ii) MOLECULE TYPE: cDNA

44 (iii) HYPOTHETICAL: NO

45 (iv) ANTI-SENSE: NO

46 (vii) IMMEDIATE SOURCE:

47 (B) CLONE: pLB001

48 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

49 ATGGTGAAGC CATCATTACC ATTCACATCC CTCTTATTCC TGCAGCTGCC CCTGCTGGGA

60

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73	GTGGGGCTGA	ACACCGACAAT	TCTGACGCC	AATGGGAATG	AAGACACCAC	AGCTGATTTC	120
75	TTCCCTGACCA	CTATGCCAC	TGACTCCCTC	AGTGTTCGA	CTCTGCCCT	CCCAGAGGTT	180
77	CAGTGTGG	TGTTCAATGT	CGAGTACATG	AATTGCACTT	GGAACAGCAG	CTCTGAGCCC	240
79	CAGCCTACCA	ACCTCACTCT	GCATTATTGG	TACAAGAACT	CGGATAATGA	TAAAGTCCAG	300
81	AAAGTGCAGCC	ACTATCTATT	CTCTGAAGAA	ATCACTCTG	GCTGTCAGTT	GCAAAAAAAG	360
83	GAGATCCACC	TCTACCAAAC	ATTGTTGTTG	CAGCTCCAGG	ACCCACGGGA	ACCCAGGAGA	420
85	CAGGCCACAC	AGATGCTAAA	ACTGCAGAA	CTGGTGATCC	CCTGGGCTCC	AGAGAACCTA	480
87	ACACTTCACA	AACTGAGTGA	ATCCCAGCTA	GAACTGAAC	GGAAACAACAG	ATTCTTGAAC	540
89	CACTGTTGG	AGCACTTGGT	GCAGTACCGG	ACTGACTGGG	ACCAACAGCTG	GACTGAACAA	600
91	TCAGTGGATT	ATAGACATAA	GTTCTCCTTG	CCTAGTGTGG	ATGGGCAGAA	ACGCTACATG	660
93	TTTCGTGTTG	GGAGCCGCTT	TAACCCACTC	TGTGGAAGTG	CTCAGCATTG	GAGTGAATGG	720
95	ACCCACCCAA	TCCACTGGGG	GAGCAATACT	TCAAAAGAGA	ATGTCGACAA	AACTCACACA	780
97	TGCCCCACCGT	GCCAGCACC	TGAACCTCC	GGGGGACCGT	CAGTCTTCCT	CTTCCCCCA	840
99	AAACCCAAGG	ACACCCCTCAT	GATCTCCCGG	ACCCCTGAGG	TCACATGCGT	GGTGGTGGAC	900
101	GTGAGCCACG	AAGACCCCTGA	GGTCAAGTTC	AACTGGTACG	TGGACGGCGT	GGAGGTGCAT	960
103	AATGCCAAGA	CAAAGCCGCG	GGAGGAGCAG	TACAACAGCA	CGTACCGTGT	GGTCAGCGTC	1020
105	CTCACCGTCC	TGCAACAGGA	CTGGCTGAAT	GGCAAGGAGT	ACAAAGTGC	GGTCTCCAAC	1080
107	AAAGCCCTCC	CAGCCCCCAT	CGAGAAAACC	ATCTCCAAAG	CCAAAGGGCA	GCCCCGAGAA	1140
109	CCACAGGTGT	ACACCCCTGCC	CCCATCCCCG	GATGAGCTGA	CCAAGAACCA	GGTCAGCCTG	1200
111	ACCTGCTGG	TCAAAGGCTT	CTATCCCAGC	GACATGCCG	TGGAGTGGGA	GAGCAATGGG	1260
113	CAGCCGGAGA	ACAACATACAA	GACCACGCT	CCCGTGTGG	ACTCCGACGG	CTCCTCTTC	1320
115	CTCTACAGCA	AGCTCACCGT	GGACAAGAGC	AGGTGGCAGC	AGGGAACGT	CTTCTCATGC	1380
117	TCCGTGATGC	ATGAGGCTCT	GCACAAACCAC	TACACGCAGA	AGAGCCTCTC	CCTGTCTCCG	1440
119	GGTAAA						1446

121 (2) INFORMATION FOR SEQ ID NO: 2:

123 (i) SEQUENCE CHARACTERISTICS:  
124 (A) LENGTH: 482 amino acids  
125 (B) TYPE: amino acid  
126 (C) STRANDEDNESS: single  
127 (D) TOPOLOGY: linear

129 (ii) MOLECULE TYPE: cDNA

131 (iii) HYPOTHETICAL: YES

133 (iv) ANTI-SENSE: NO

138 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

140	Met	Val	Lys	Pro	Ser	Leu	Pro	Phe	Thr	Ser	Leu	Leu	Phe	Leu	Gln	Leu
141	1					5				10					15	
143	Pro	Leu	Leu	Gly	Val	Gly	Leu	Asn	Thr	Thr	Ile	Leu	Thr	Pro	Asn	Gly
144							20			25					30	
146	Asn	Glu	Asp	Thr	Thr	Ala	Asp	Phe	Phe	Leu	Thr	Thr	Met	Pro	Thr	Asp
147							35			40					45	
149	Ser	Leu	Ser	Val	Ser	Thr	Leu	Pro	Leu	Pro	Glu	Val	Gln	Cys	Phe	Val
150							50			55					60	
152	Phe	Asn	Val	Glu	Tyr	Met	Asn	Cys	Thr	Trp	Asn	Ser	Ser	Ser	Glu	Pro
153						65			70			75			80	
155	Gln	Pro	Thr	Asn	Leu	Thr	Leu	His	Tyr	Trp	Tyr	Lys	Asn	Ser	Asp	Asn
156							85			90					95	
158	Asp	Lys	Val	Gln	Lys	Cys	Ser	His	Tyr	Leu	Phe	Ser	Glu	Glu	Ile	Thr
159							100			105					110	
161	Ser	Gly	Cys	Gln	Leu	Gln	Lys	Lys	Glu	Ile	His	Leu	Tyr	Gln	Thr	Phe

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162	115	120	125
164	Val Val Gln Leu Gln Asp Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln		
165	130	135	140
167	Met Leu Lys Leu Gln Asn Leu Val Ile Pro Trp Ala Pro Glu Asn Leu		
168	145	150	155
170	Thr Leu His Lys Leu Ser Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn		160
171	165	170	175
173	Arg Phe Leu Asn His Cys Leu Glu His Leu Val Gln Tyr Arg Thr Asp		
174	180	185	190
176	Trp Asp His Ser Trp Thr Glu Gln Ser Val Asp Tyr Arg His Lys Phe		
177	195	200	205
179	Ser Leu Pro Ser Val Asp Gly Gln Lys Arg Tyr Met Phe Arg Val Arg		
180	210	215	220
182	Ser Arg Phe Asn Pro Leu Cys Gly Ser Ala Gln His Trp Ser Glu Trp		
183	225	230	235
185	Ser His Pro Ile His Trp Gly Ser Asn Thr Ser Lys Glu Asn Val Asp		240
186	245	250	255
188	Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly		
189	260	265	270
191	Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile		
192	275	280	285
194	Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu		
195	290	295	300
197	Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His		
198	305	310	315
200	Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg		
201	325	330	335
203	Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys		
204	340	345	350
206	Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu		
207	355	360	365
209	Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr		
210	370	375	380
212	Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu		
213	385	390	395
215	400	405	410
216	415		
218	Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val		
219	420	425	430
221	Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp		
222	435	440	445
224	Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His		
225	450	455	460
227	Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro		
228	465	470	475
230	480		
	Gly Lys		
232	(2) INFORMATION FOR SEQ ID NO: 3:		
234	(i) SEQUENCE CHARACTERISTICS:		
235	(A) LENGTH: 112 amino acids		

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236 (B) TYPE: amino acid  
237 (C) STRANDEDNESS:  
238 (D) TOPOLOGY: linear  
240 (ii) MOLECULE TYPE: peptide  
242 (v) FRAGMENT TYPE: internal  
247 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
249 Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser  
250 1 5 10 15  
252 Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Tyr Gly Val His  
253 20 25 30  
255 Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile  
256 35 40 45  
258 Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met Ser Arg Leu  
259 50 55 60  
261 Asn Ile Asn Arg Asp Asn Ser Lys Ser Gln Ile Phe Leu Lys Met Asn  
262 65 70 75 80  
264 Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Glu Gly  
265 85 90 95  
267 Ser Thr Val Asp Ser Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr  
268 100 105 110

271 (2) INFORMATION FOR SEQ ID NO: 4:  
273 (i) SEQUENCE CHARACTERISTICS:  
274 (A) LENGTH: 106 amino acids  
275 (B) TYPE: amino acid  
276 (C) STRANDEDNESS: not relevant  
277 (D) TOPOLOGY: linear  
279 (ii) MOLECULE TYPE: peptide  
281 (v) FRAGMENT TYPE: internal  
286 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

288 Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly  
289 1 5 10 15  
291 Asp Ser Ile Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Thr Thr Ala  
292 20 25 30  
294 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile  
295 35 40 45  
297 Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly  
298 50 55 60  
300 Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Val Gln Ala  
301 65 70 75 80  
303 Glu Asp Leu Ala Leu Tyr Tyr Cys Gln Gln His Tyr Ile Thr Pro Trp  
304 85 90 95  
306 Thr Phe Gly Gly Thr Lys Leu Glu Ile  
307 100 105

309 (2) INFORMATION FOR SEQ ID NO: 5:  
311 (i) SEQUENCE CHARACTERISTICS:  
312 (A) LENGTH: 319 base pairs  
313 (B) TYPE: nucleic acid  
314 (C) STRANDEDNESS: single  
315 (D) TOPOLOGY: linear

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317	(ii) MOLECULE TYPE: cDNA	
322	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:	
324	GATATCGTAA TGACCCAGTC TCACAAATTG ATGTCCACAT CAGTAGGAGA CAGTATCACC	60
326	ATCACCTGCA AGGCCAGTCA GGATGTGACT ACTGCTGTAG CCTGGTATCA ACAAAACCA	120
328	GGGCAATCTC CTAAACATTCT GATTTACTGG GCATCCACCC GGCACACTGG AGTCCCTGAT	180
330	CGCTTCACAG GCAGTGGATC TGGGACAGAT TATACTCTCA CCATCAGCAG TGTGCAGGCT	240
332	GAAGACCTGG CACTTTATTA CTGTCAGCAA CATTATATCA CTCCGTGGAC GTTCGGTGGA	300
334	GGGACCAAGC TGGAGATCT	319
336	(2) INFORMATION FOR SEQ ID NO: 6:	
338	(i) SEQUENCE CHARACTERISTICS:	
339	(A) LENGTH: 336 base pairs	
340	(B) TYPE: nucleic acid	
341	(C) STRANDEDNESS: single	
342	(D) TOPOLOGY: linear	
344	(ii) MOLECULE TYPE: cDNA	
349	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:	
351	CTGCAGGAGT CAGGACCTGG CCTGGTGGCG CCCTCACAGA GCCTGTCCAT CACTTGCAC	60
353	GTCTCTGGGT TTTCATTAAC CAGCTATGGT GTACACTGGG TTCGCCAGCC TCCAGGAAAG	120
355	GGTCTGGAGT GGCTGGGAGT CATTGGGCT GGTGGAAGCA CAAATTATAA TTCGGCTCTC	180
357	ATGTCCAGAC TGAACATCAA CAGAGACAAT TCCAAGAGCC AAATTTCTT AAAATGAAC	240
359	AGTCTGAAA CTGATGACAC AGCCATCTAC TACTGTGCCA GAGAGGGTTC TACGGTAGAT	300
361	TCTATGGACT ACTGGGGCCA AGGGACCACG GTCACC	336
363	(2) INFORMATION FOR SEQ ID NO: 7:	
365	(i) SEQUENCE CHARACTERISTICS:	
366	(A) LENGTH: 36 base pairs	
367	(B) TYPE: nucleic acid	
368	(C) STRANDEDNESS: single	
369	(D) TOPOLOGY: linear	
371	(ii) MOLECULE TYPE: cDNA	
376	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:	
378	AACTGCAGCG GCCGCCATGG TGAAGCCATC ATTACC	36
380	(2) INFORMATION FOR SEQ ID NO: 8:	
382	(i) SEQUENCE CHARACTERISTICS:	
383	(A) LENGTH: 32 base pairs	
384	(B) TYPE: nucleic acid	
385	(C) STRANDEDNESS: single	
386	(D) TOPOLOGY: linear	
388	(ii) MOLECULE TYPE: cDNA	
393	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:	
395	GACTTTGTCTG ACATTCTCTT TTGAAGTATT GC	32
397	(2) INFORMATION FOR SEQ ID NO: 9:	
399	(i) SEQUENCE CHARACTERISTICS:	
400	(A) LENGTH: 27 base pairs	
401	(B) TYPE: nucleic acid	
402	(C) STRANDEDNESS: single	
403	(D) TOPOLOGY: linear	
405	(ii) MOLECULE TYPE: cDNA	
410	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:	
412	CTGGATATCG TAATGACCCA GTCTCCA	27

VERIFICATION SUMMARY  
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L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]